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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/879,959

DATE: 10/01/2001
 TIME: 10:39:26

Input Set : A:\PTO_VSK.txt
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3 <110> APPLICANT: Weigel, Paul H
 4 Kumari, Kshama
 5 DeAngelis, Paul
 7 <120> TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND
 EXPRESSION THEREOF

8 IN BACILLUS SUBTILIS
 10 <130> FILE REFERENCE: 3554.049
 12 <140> CURRENT APPLICATION NUMBER: US 09/879,959
 C--> 13 <141> CURRENT FILING DATE: 2001-09-12
 15 <150> PRIOR APPLICATION NUMBER: 09/469,200
 16 <151> PRIOR FILING DATE: 1999-12-21
 18 <150> PRIOR APPLICATION NUMBER: 09/178,851
 19 <151> PRIOR FILING DATE: 1998-10-26
 21 <160> NUMBER OF SEQ ID NOS: 10
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1254
 27 <212> TYPE: DNA

ENTERED

28 <213> ORGANISM: Streptococcus equisimilis
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 33 atttacgtca atgtttatct ctttggtgct aaaggaagct tgtcaattta tggctTTTTtg 120
 35 ctgatatgctt acctattagt caaaatgtcc ttatcctttt ttacaagcc atttaaggga 180
 37 agggctgggc aatataaggt tgcagccatt attcctctt ataacgaaga tgctgagtca 240
 39 ttgctagaga ccttaaaaag tgttcagcag caaacctatc ccctagcaga aatttatgtt 300
 41 gttgacgatg gaagtgtgta tgagacaggt attaaagcga ttgaagacta tgtgcgtgac 360
 43 actggtgacc tatcaagcaa tgtcattgtt catcggtcag agaaaaatca aggaaagcgt 420
 45 catgcacagg cctgggcctt tgaaagatca gacgctgatg tctTTTTtgac cgttgactca 480
 47 gatacttata tctaccctga tgcttttagag gagttgttaa aaacctttaa tgacccaact 540
 49 gttttttgctg cgacgggtca ccttaatgtc agaaatagac aaaccaatct cttaacacgc 600
 51 ttgacagata ttgctatga taatgctttt ggcgttgaac gagctgcca atccgttaca 660
 53 ggtaatatcc ttgtttgctc aggtccgctt agcgtttaca gacgcgaggt ggttgttcct 720
 55 aacatagata gatacatcaa ccagaccttc ctgggtattc ctgtaagtat tggatgatgac 780
 57 aggtgcttga ccaactatgc aactgattta ggaaagactg tttatcaatc cactgctaaa 840
 59 tgtattacag atgttcctga caagatgtct acttacttga agcagcaaaa ccgctggaac 900
 61 aagtccttct ttagagagtc cattatttct gttaagaaaa tcatgaacaa tcctttttgta 960
 63 gccctatgga ccatacttga ggtgtctatg tttatgatgc ttgtttattc tgtggtggat 1020
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 67 atcttcattg ttgcctgtg tcggaacatt cattacatgc ttaagcacc gctgtccttc 1140
 69 ttgttatctc cgttttatgg ggtgctgcat ttgtttgtcc tacagccctt gaaattatat 1200
 71 tctcttttta ctattagaaa tgctgactgg ggaacacgta aaaaattatt ataa 1254

74 <210> SEQ ID NO: 2
 75 <211> LENGTH: 417
 76 <212> TYPE: PRT
 77 <213> ORGANISM: Streptococcus equisimilis
 79 <400> SEQUENCE: 2
 81 Met Arg Thr Leu Lys Asn Leu Ile Thr Val Val Ala Phe Ser Ile Phe
 82 1 5 10 15

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85 Trp Val Leu Leu Ile Tyr Val Asn Val Tyr Leu Phe Gly Ala Lys Gly
86          20          25          30
89 Ser Leu Ser Ile Tyr Gly Phe Leu Leu Ile Ala Tyr Leu Leu Val Lys
90          35          40          45
93 Met Ser Leu Ser Phe Phe Tyr Lys Pro Phe Lys Gly Arg Ala Gly Gln
94          50          55          60
97 Tyr Lys Val Ala Ala Ile Ile Pro Ser Tyr Asn Glu Asp Ala Glu Ser
98 65          70          75          80
101 Leu Leu Glu Thr Leu Lys Ser Val Gln Gln Gln Thr Tyr Pro Leu Ala
102          85          90          95
105 Glu Ile Tyr Val Val Asp Asp Gly Ser Ala Asp Glu Thr Gly Ile Lys
106          100          105          110
109 Arg Ile Glu Asp Tyr Val Arg Asp Thr Gly Asp Leu Ser Ser Asn Val
110          115          120          125
113 Ile Val His Arg Ser Glu Lys Asn Gln Gly Lys Arg His Ala Gln Ala
114          130          135          140
117 Trp Ala Phe Glu Arg Ser Asp Ala Asp Val Phe Leu Thr Val Asp Ser
118 145          150          155          160
121 Asp Thr Tyr Ile Tyr Pro Asp Ala Leu Glu Glu Leu Leu Lys Thr Phe
122          165          170          175
125 Asn Asp Pro Thr Val Phe Ala Ala Thr Gly His Leu Asn Val Arg Asn
126          180          185          190
129 Arg Gln Thr Asn Leu Leu Thr Arg Leu Thr Asp Ile Arg Tyr Asp Asn
130          195          200          205
133 Ala Phe Gly Val Glu Arg Ala Ala Gln Ser Val Thr Gly Asn Ile Leu
134          210          215          220
137 Val Cys Ser Gly Pro Leu Ser Val Tyr Arg Arg Glu Val Val Val Pro
138 225          230          235          240
141 Asn Ile Asp Arg Tyr Ile Asn Gln Thr Phe Leu Gly Ile Pro Val Ser
142          245          250          255
145 Ile Gly Asp Asp Arg Cys Leu Thr Asn Tyr Ala Thr Asp Leu Gly Lys
146          260          265          270
149 Thr Val Tyr Gln Ser Thr Ala Lys Cys Ile Thr Asp Val Pro Asp Lys
150          275          280          285
153 Met Ser Thr Tyr Leu Lys Gln Gln Asn Arg Trp Asn Lys Ser Phe Phe
154          290          295          300
157 Arg Glu Ser Ile Ile Ser Val Lys Lys Ile Met Asn Asn Pro Phe Val
158 305          310          315          320
161 Ala Leu Trp Thr Ile Leu Glu Val Ser Met Phe Met Met Leu Val Tyr
162          325          330          335
165 Ser Val Val Asp Phe Phe Val Gly Asn Val Arg Glu Phe Asp Trp Leu
166          340          345          350
169 Arg Val Leu Ala Phe Leu Val Ile Ile Phe Ile Val Ala Leu Cys Arg
170          355          360          365
173 Asn Ile His Tyr Met Leu Lys His Pro Leu Ser Phe Leu Leu Ser Pro
174          370          375          380
177 Phe Tyr Gly Val Leu His Leu Phe Val Leu Gln Pro Leu Lys Leu Tyr
178 385          390          395          400
181 Ser Leu Phe Thr Ile Arg Asn Ala Asp Trp Gly Thr Arg Lys Lys Leu

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185 Leu
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190 <211> LENGTH: 22
191 <212> TYPE: DNA
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199 <211> LENGTH: 20
200 <212> TYPE: DNA
201 <213> ORGANISM: Streptococcus equisimilis
203 <400> SEQUENCE: 4
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208 <211> LENGTH: 20
209 <212> TYPE: DNA
210 <213> ORGANISM: Streptococcus equisimilis
212 <400> SEQUENCE: 5
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217 <211> LENGTH: 17
218 <212> TYPE: DNA
219 <213> ORGANISM: Streptococcus equisimilis
221 <400> SEQUENCE: 6
222 tttttacgtg ttcccca                17
225 <210> SEQ ID NO: 7
226 <211> LENGTH: 567
227 <212> TYPE: PRT
228 <213> ORGANISM: Chlorella virus PBCV-1
230 <400> SEQUENCE: 7
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233 1          5          10          15
236 Ser Asn Leu Ile Ala Val Gly Gly Ala Ser Leu Ile Leu Ala Pro Ala
237          20          25          30
240 Ile Thr Gly Tyr Val Leu His Trp Asn Ile Ala Leu Ser Thr Ile Trp
241          35          40          45
244 Gly Val Ser Ala Tyr Gly Ile Phe Val Phe Gly Phe Phe Leu Ala Gln
245          50          55          60
248 Val Leu Phe Ser Glu Leu Asn Arg Lys Arg Leu Arg Lys Trp Ile Ser
249 65          70          75          80
252 Leu Arg Pro Lys Gly Trp Asn Asp Val Arg Leu Ala Val Ile Ile Ala
253          85          90          95
256 Gly Tyr Arg Glu Asp Pro Tyr Met Phe Gln Lys Cys Leu Glu Ser Val
257          100         105         110
260 Arg Asp Ser Asp Tyr Gly Asn Val Ala Arg Leu Ile Cys Val Ile Asp
261          115         120         125
264 Gly Asp Glu Asp Asp Asp Met Arg Met Ala Ala Val Tyr Lys Ala Ile
265          130         135         140

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268 Tyr Asn Asp Asn Ile Lys Lys Pro Glu Phe Val Leu Cys Glu Ser Asp
269 145                      150                      155                      160
272 Asp Lys Glu Gly Glu Arg Ile Asp Ser Asp Phe Ser Arg Asp Ile Cys
273                      165                      170                      175
276 Val Leu Gln Pro His Arg Gly Lys Arg Glu Cys Leu Tyr Thr Gly Phe
277                      180                      185                      190
280 Gln Leu Ala Lys Met Asp Pro Ser Val Asn Ala Val Val Leu Ile Asp
281                      195                      200                      205
284 Ser Asp Thr Val Leu Glu Lys Asp Ala Ile Leu Glu Val Val Tyr Pro
285                      210                      215                      220
288 Leu Ala Cys Asp Pro Glu Ile Gln Ala Val Ala Gly Glu Cys Lys Ile
289 225                      230                      235                      240
292 Trp Asn Thr Asp Thr Leu Leu Ser Leu Leu Val Ala Trp Arg Tyr Tyr
293                      245                      250                      255
296 Ser Ala Phe Cys Val Glu Arg Ser Ala Gln Ser Phe Phe Arg Thr Val
297                      260                      265                      270
300 Gln Cys Val Gly Gly Pro Leu Gly Ala Tyr Lys Asp Ile Ile Lys Glu
301                      275                      280                      285
304 Ile Lys Asp Pro Trp Ile Ser Gln Arg Phe Leu Gly Gln Lys Cys Thr
305                      290                      295                      300
308 Tyr Gly Asp Asp Arg Arg Leu Thr Asn Glu Ile Leu Met Arg Gly Lys
309 305                      310                      315                      320
312 Lys Val Val Phe Thr Pro Phe Ala Val Gly Trp Ser Asp Ser Pro Thr
313                      325                      330                      335
316 Asn Val Phe Arg Tyr Ile Val Gln Gln Thr Arg Trp Ser Lys Ser Trp
317                      340                      345                      350
320 Cys Arg Glu Ile Trp Tyr Thr Leu Phe Ala Ala Trp Lys His Gly Leu
321                      355                      360                      365
324 Ser Gly Ile Trp Leu Ala Phe Glu Cys Leu Tyr Gln Ile Thr Tyr Phe
325                      370                      375                      380
328 Phe Leu Val Ile Tyr Leu Phe Ser Arg Leu Ala Val Glu Ala Asp Pro
329 385                      390                      395                      400
332 Arg Ala Gln Thr Ala Thr Val Ile Val Ser Thr Thr Val Ala Leu Ile
333                      405                      410                      415
336 Lys Cys Gly Tyr Phe Ser Phe Arg Ala Lys Asp Ile Arg Ala Phe Tyr
337                      420                      425                      430
340 Phe Val Leu Tyr Thr Phe Val Tyr Phe Phe Cys Met Ile Pro Ala Arg
341                      435                      440                      445
344 Ile Thr Ala Met Met Thr Leu Trp Asp Ile Gly Trp Asp Thr Arg Gly
345                      450                      455                      460
348 Gly Asn Glu Lys Pro Ser Val Gly Thr Arg Val Ala Leu Trp Ala Lys
349 465                      470                      475                      480
352 Gln Tyr Leu Ile Ala Tyr Met Trp Trp Ala Ala Val Val Gly Ala Gly
353                      485                      490                      495
356 Val Tyr Ser Ile Val His Asn Trp Met Phe Asp Trp Asn Ser Leu Ser
357                      500                      505                      510
360 Tyr Arg Phe Ala Leu Val Gly Ile Cys Ser Tyr Ile Val Phe Ile Val
361                      515                      520                      525
364 Ile Val Leu Val Val Tyr Phe Thr Gly Lys Ile Thr Thr Trp Asn Phe

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365      530      535      540
368 Thr Lys Leu Gln Lys Glu Leu Ile Glu Asp Arg Val Leu Tyr Asp Ala
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376 <210> SEQ ID NO: 8
377 <211> LENGTH: 1740
378 <212> TYPE: DNA
379 <213> ORGANISM: Chlorella virus PBCV-1
381 <400> SEQUENCE: 8
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386 ctgggtatgt tctacattgg aatattgctc tctcgacaat ctggggagta tcagcttatg      180
388 gtattttcgt ttttgggttt ttccttgcac aagttttatt ttcagaactg aacaggaaac      240
390 gtcttcgcaa gtggatttct ctcagacctc aggggttgaa tgatgttcgt ttggctgtga      300
392 tcattgctgg atatcgcgag gatccttata tgttccagaa gtgcctcgag tctgtacgtg      360
394 actctgatta tggcaacggt gcccgctctga tttgtgtgat tgacggtgat gaggacgatg      420
396 atatgaggat ggctgccgtt tacaaggcga tctacaatga taatatcaag aagcccgagt      480
398 ttgttctgtg tgagtcagac gacaaggaag gtgaacgcac cgactctgat ttctctcgcg      540
400 acatttgtgt cctccagcct catcgtggaa aacgggagtg tctttatact gggtttcaac      600
402 ttgcaaagat ggaccccagt gtcaatgctg tcgttctgat tgacagcgat accgttctcg      660
404 agaaggatgc tattctggaa gttgtatacc cacttgcatg cgatcccgag atccaagccg      720
406 ttgcaggatga gtgtaagatt tggaaacacag acactctttt gagtcttctc gtcgcttggc      780
408 ggtactattc tgcgttttgt gtggagagga gtgccagtc ttttttcagg actgttcagt      840
410 gcgttggggg gccactgggt gcctacaaga ttgatatacat taaggagatt aaggaccctt      900
412 ggatttccca gcgctttctt ggtcagaagt gtacttacgg tgacgaccgc cggctaacca      960
414 acgagatctt gatgcgtggt aaaaagggtg tgttcaactcc atttgctgtt ggttggctctg      1020
416 acagtccgac caatgtgttt cgggtacatcg ttcagcagac ccgctggagt aagtcgtggt      1080
418 gccgcgaaat ttggtacacc ctcttcgccg cgtggaagca cggtttgtct ggaatttggc      1140
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422 gcctagccgt tgaggccgac cctcgcgccc agacagccac ggtgattgtg agcaccacgg      1260
424 ttgcattgat taagtgtggg tatttttcat tccgagccaa ggatattcgg gcgttttact      1320
426 ttgtgcttta tacatttgtt tactttttct gtatgattcc ggccaggatt actgcaatga      1380
428 tgacgctttg ggacattggc tgggatactc gcggtggaaa cgagaagcct tccgttggca      1440
430 cccgggtcgc tctgtgggca aagcaatata tcattgcata tatgtggtgg gccgcggtg      1500
432 ttggcgctgg agtttacagc atcgtccata actggatggt cgattggaat tctctttctt      1560
434 atcgttttgc tttggttggg atttggttctt acattgtttt tattgttatt gtgctggtgg      1620
436 tttatttcac cggcaaaatt acgacttgga atttcacgaa gcttcagaag gagctaatac      1680
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442 <211> LENGTH: 2937
443 <212> TYPE: DNA
444 <213> ORGANISM: pasteurilla multocida
446 <400> SEQUENCE: 9
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451 gttgaatttc aaattaccaa atgccaagaa aaactctcag cacatccttc tgttaattca      180
453 gcacatcttt ctgtaaataa agaagaaaaa gtcaatgttt gcgatagtcg gttagatatt      240
455 gcaacacaac tgttactttc caacgtaaaa aaattagtag tttctgactc ggaaaaaac      300

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date